

TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT

234

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 590 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

ACTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA      60
ATTGATAGC AATATTTTGG AGATTACAGA GTTTTAGTAA TTACCAATTA CACAGTAAA      120
AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA      180
TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA      240
AAAGCTTTCA AAANAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT      300
CAGGATAAAN AACTGAAGGG CANAAAGAAT TAATTTTCAC TTCATGTAAC NCACCCANAT      360
TTACAATGGC TTAAATGCAN GGAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC      420
TGGTCTCTAA TCTGCCTTAC TCTTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG      480
GGCTCCTGTT ATATCCACAA TCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT      540
GCCTTCCTTT GAGGAGACTT CATCTACTG GCCAACACTC AGTCACATGT      590

```

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 774 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTTAAAG AAGGAAAAAA AACGAGGCC      60
TGAACAGAAT TTTCCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGA GGTCAAGAC      120
GCTTCACTGC TTGAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG      180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCCAA      240
AACATCAAAG AAAGGAAGGT GGCCTCATACT CCCCAGCCT ACACAGTTCT CCAGGGCTCT      300
CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCCCAGG CTCCTGTGTG      360
CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCACC CTCTGCTGAT CCTGCGTGGC      420
CCACTCTCT TGAACACACA TCCCAGGTT ATATTCTGG ACATGGCTGA ACCTCCTATT      480
CCTACTTCG AGATGCCTTG CTCCCTGCAG CCTGTCAAAA TCCCCTCAC CCTCCAAACC      540
ACGGCATGGG AAGCCTTTCT GACTTGCCTG ATTACTCCAG CATCTTGGAA CAATCCCTGA      600
TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC      660
AGGCTGCTGG CTTCAAATTN TGGCTATTG ACGAGCTATG GGACCTTGGG CAAGTNATCT      720
TCACTTCTAT GGGCTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT      774

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(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification ⁶ : C07K 14/00, A61K 39/00</p>	<p>A2</p>	<p>(11) International Publication Number: WO 98/37093 (43) International Publication Date: 27 August 1998 (27.08.98)</p>
<p>(21) International Application Number: PCT/US98/03492 (22) International Filing Date: 25 February 1998 (25.02.98) (30) Priority Data: 08/806,099 25 February 1997 (25.02.97) US 08/904,804 1 August 1997 (01.08.97) US 09/020,956 9 February 1998 (09.02.98) US (71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US). (72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US). (74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).</p>		<p>(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p>Published Without international search report and to be republished upon receipt of that report.</p>
<p>(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE (57) Abstract Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.</p>		

121

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ACCCAAAAAT CCAATGCTGA ATATTGGCT TCATTATTC CANATTCTTT GATTGTCAAA 60
GGATTTAATG TTGTCTCAGC TTGGGCACTT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG 120
GTTTATATAT GCAGCAACAA TATTCAAGCG GCACAACAGG TTATTGAACT TGCCCGCCAG 180
TTNAATTTC TTTCCATTGA CTGGGATCC TTATCATCAG CCAGAGAGAT TGAAAATTTA 240
CCCCTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTGGGCCACA 300
TTTTTTTTTC CTTTATTCCT TTGTCAGA 328

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(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

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ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AACTGAATT CTCTCCAGTT 60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT 120
CATTATGCCA AAGGANATAT ACATTTCAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT 180
TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT 240
TCTCATCGGT 250

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(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

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ACCCAGAATC CAATGCTGAA TATTTGGCTT CATTATCCC AGATTCTTTG ATTGTCAAAG 60
GATTTAATGT TGTCTCAGCT TGGGCACTTC AGTTAGGACC TAAGGATGCC AGCCGGCAGG 120
TTTATATATG CAGCAACAAT ATTCAAGCGC GACAACAGGT TATTGAACTT GCCCGCCAGT 180
TGAATTCAT TCCCATGAC TTGGGATCCT TATCATCAGC CANAGAGATT GAAAATTAC 240
CCCTACGACT CTTTACTCTC TGGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT 300
TTTTTTTCC TTTATTCCTT TGTGAGAGAT GCGATTCATC CATATGCTAN AAACCAACAG 360
AGTGACTTTT AAAAAATTCC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT 420
ACTTTGCTCT CCTAATATA CCTC 444

```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AACTGAATT CTCTCCAGTT 60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT 120

```

122

CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT 180
 TTCAATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT 240
 TCTCATCGGT AAGCAGAGGC TGTAGGCAAC ATGGACCATA GCGAANAAAA AACTTAGTAA 300
 TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCAA GGTGGAAATC TCCTATACTT 360
 GGTGCC 366

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC AGAACTCCAC TGCANGAGGG AGGGCCGGGC CAGGAGAATC TCCGCTTGTC 60
 CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNTAA GGGCTNTNC ATTTTITAT 120
 TAATAAAAAG TNNAAGGCT CTCTTCTCAA CTTTTTCCC TTNGGCTGGA AAATTTAAAA 180
 ATCAAAAATT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT 240
 AATTCTTCTT TCCCTCTTT 260

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTTCAGGAA NAGGAACGCA TATAATTGTA 60
 TCTTGCTAT AATTTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGGAAATGTAG 120
 GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTTT 180
 ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATTT ATAATTAGCC ACTTACCCTA 240
 ATATCCTTCA TGCTTGTAAG GT 262

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCAATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA 60
 CCCCTATCAA CTCCTTTTG TAGTAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC 120
 AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGCT TGCTAGGAAA 180
 ANAAATCAGC AGACACAGGT GTAAA 205

(2) INFORMATION FOR SEQ ID NO:219:

Hit [ENTER] to continue

NA_SEQUENCE 1.0

ID AA447322 standard; RNA; EST; 618 BP.

XX

AC AA447322;

XX

SV AA447322,1

XX

DT 07-APR-1998 (Rel. 55, Created).

DT 07-APR-1998 (Rel. 55, Last updated, Version 1)

XX

DE SA.C08R PN001-Normal Human Prostate Homo sapiens cDNA clone SA.C08

DE 5'.

XX

KW EST.

XX

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;

OC Primates; Catarrhini; Hominidae; Homo.

XX

RN [1]

RP 1-618

RX MEDLINE; 98126432.

RA Nelson P.S., Ng W.-L., Schummer M., True L.D., Liu A.L., Bumgarner R.,

RA Ferguson C., Dimak A., Hood L.;

RT "An expressed-sequence-tag database of the human prostate: sequence

RT analysis of 1168 cDNA clones";

RL Genomics 47(1):12-25(1998).

XX

CC Contact: Nelson PS

CC Department of Molecular Biotechnology

CC University of Washington

CC Box 357730, HSB K360, 1705 NE Pacific, Seattle, WA 98195, USA

CC Tel: 206 685 7336

CC Fax: 206 685 7301

CC Email: psnells@u.washington.edu

CC Seq primer: M13 Reverse.

XX

FH Key Location/Qualifiers

FH

FT source 1. .618

FT /db_xref="taxon:9606"

FT /db_xref="ESTLIB:876"

FT /note="Organ: prostate; Vector: pSport1; Site_1: Not1;

FT Site_2: Sall; PolyA+ RNA was isolated from the prostate of

FT a healthy 25 year old male organ donor. 1st strand cDNA

FT was primed with oligo(dT)Not1. Double-stranded cDNA was

FT ligated to Sall adapters and directionally cloned into

FT pSport1 (Life Technologies). Average insert size is 1.1kb."

FT /sex="male"

FT /organism="Homo sapiens"

FT /clone="SA.C08"

FT /clone_lib="PN001-Normal Human Prostate"

XX

SQ Sequence 618 BP; 165 A; 141 C; 118 G; 192 T; 2 other;

Aa447322 Length: 618 November 9, 1999 11:49 Type: N Check: 7801 ..

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1 CGACCCACGC GTCCGCCACG CGTCCGGCTT AATTTTCAGAG ATTCTTTCCA
51 TATGTTACTA AAAAAATGTTT TGTTTCAGCCT AACATACTGA GTTTTTTTTA
101 ACTTTCTAAA TTATTGAATT TCCATCATGC ATTCATCCAA AATTAAGGCA
151 GACTGTTTGG ATTCTTCCAG TGGCCAGATG AGCTAAATTA AATCACAAAA
201 GCAGATGCTT TTGTATGATC TCCAAATTGC CAACTTTAAG GAAATATTCT
251 CTTGAAATTG TCTTTAAAGA TCTTTTGCAG CTTTGCAGAT ACCCAGACTG
301 AGCTGGAACT GGAATTTGTC TTCCTATTGA CTCTACTTCT TTAAAAGCGG
351 CTGCCCATTG CATTCTCAG CTGTCCTTGC AGTTAGGTGT ACATGTGACT
401 GAGTGTGGC CAGTGAGATG AAGTCTCCTC AAAGGAAGGC AGCATGTGTC
451 CTTTTTCATC CCNGCATCTT GCTGCTGGGA TTGTGGATAT AACAGGAGCC
501 CTGGCAGCTG TCTCCAGAGG ATCAAAGCCA CACCCAAAGA GTAAGGCA
551 TTAGAGACCA GANAGACCTT GACTACTTCC CTACTTCCAC TGCTTTTTCC
601 TGCATTAAGC CATGTAAA

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Hit [ENTER] to continue

NA_SEQUENCE 1.0

ID AA447322 standard; RNA; EST; 618 BP.

XX

AC AA447322;

XX

SV AA447322,1

XX

DT 07-APR-1998 (Rel. 55, Created).

DT 07-APR-1998 (Rel. 55, Last updated, Version 1)

XX

DE SA.C08R PN001-Normal Human Prostate Homo sapiens cDNA clone SA.C08

DE

5'.

XX

KW EST.

XX

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;

OC Primates; Catarrhini; Hominidae; Homo.

XX

RN [1]

RP 1-618

RX MEDLINE; 98126432.

RA Nelson P.S., Ng W.-L., Schummer M., True L.D., Liu A.L., Bumgarner R.,

RA Ferguson C., Dimak A., Hood L.;

RT "An expressed-sequence-tag database of the human prostate: sequence

RT analysis of 1168 cDNA clones";

RL Genomics 47(1):12-25(1998).

XX

CC Contact: Nelson PS

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CC Box 357730, HSB K360, 1705 NE Pacific, Seattle, WA 98195, USA

CC Tel: 206 685 7336

CC Fax: 206 685 7301

CC Email: psnelse@u.washington.edu

CC Seq primer: M13 Reverse.

XX

FH Key Location/Qualifiers

FH

FT source 1. .618

FT /db_xref="taxon:9606"

FT /db_xref="ESTLIB:876"

FT /note="Organ: prostate; Vector: pSport1; Site_1: Not1;

FT Site_2: Sall; PolyA+ RNA was isolated from the prostate of

FT a healthy 25 year old male organ donor. 1st strand cDNA

FT was primed with oligo(dT)Not1. Double-stranded cDNA was

FT ligated to Sall adapters and directionally cloned into

FT pSport1 (Life Technologies). Average insert size is 1.1kb."

FT /sex="male"

FT /organism="Homo sapiens"

FT /clone="SA.C08"

FT /clone_lib="PN001-Normal Human Prostate"

XX

SQ Sequence 618 BP; 165 A; 141 C; 118 G; 192 T; 2 other;

Aa447322 Length: 618 November 9, 1999 11:49 Type: N Check: 7801 ..

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1 CGACCCACGC GTCCGCCACG CGTCCGGCTT AATTCAGAG ATTCTTTCCA
51 TATGTTACTA AAAAATGTTT TGTTTCAGCCT AACATACTGA GTTTTTTTTA
101 ACTTTCTAAA TTATTGAATT TCCATCATGC ATTCATCCAA AATTAAGGCA
151 GACTGTTTGG ATTCTTCCAG TGGCCAGATG AGCTAAATTA AATCACAAAA
201 GCAGATGCTT TTGTATGATC TCCAAATTGC CAACTTTAAG GAAATATTCT
251 CTTGAAATTG TCTTTAAAGA TCTTTTGCAG CTTTGCAGAT ACCCAGACTG
301 AGCTGGAAC T GGAATTTGTC TTCCTATTGA CTCTACTTCT TTAAAAGCGG
351 CTGCCCATT A CATTCTCAG CTGTCCTTGC AGTTAGGTGT ACATGTGACT
401 GAGTGTGGC CAGTGAGATG AAGTCTCCTC AAAGGAAGGC AGCATGTGTC
451 CTTTTTCATC CCNGCATCTT GCTGCTGGGA TTGTGGATAT AACAGGAGCC

501 CTGGCAGCTG TCTCCAGAGG ATCAAAGCCA CACCCAAAGA GTAAGGCA
551 TTAGAGACCA GANAGACCTT GACTACTTCC CTACTTCCAC TGCTTTTTCC
601 TGCATTAAGC CATGTAAA

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